

60 *

TGTGGGTTTCG AATTTTACCC ACCACAAGTT TTGTCTTACC ATAATTGGGA TAAGGAGTCT

120 *

AATTTCCCTT GTACAATTTT CCAATTTCTT CCTCCGCCAC ACCATATATA TACTGTACGC

180 *

CACTTCGAAC GCTACAATGT TTGAAAAAAG ACGCAGATTT TACAAAGACG GAGAAGATAA

TAAGCTTCAA GTACTCCGAT CGTCAGGTGG CCTTTGGAAG CCAACAAACT GGCT ATG
Met

240 *

GCT CTT TCT CTT CAC ACT GTA TTT CTC TGC AAA GAG GAA GCC CTC AAT
Ala Leu Ser Leu His Thr Val Phe Leu Cys Lys Glu Glu Ala Leu Asn

300 *

TTA TAT GCA AGA TCA CCA TGT AAT GAA AGG TTT CAC AGG AGT GGA CAA
Leu Tyr Ala Arg Ser Pro Cys Asn Glu Arg Phe His Arg Ser Gly Gln

360 *

CCT CCT ACC AAC ATA ATC ATG ATG AAA ATT CGA TCC AAC AAT GGA TAT
Pro Pro Thr Asn Ile Ile Met Met Lys Lys Ile Arg Ser Asn Asn Gly Tyr

420 *

TTT AAT TCT TTC CGG TTG TTT ACA TCT TAT AAG ACA AGT TCT TTC TCA
Phe Asn Ser Phe Arg Leu Phe Thr Ser Tyr Lys Thr Ser Ser Phe Ser

FIGURE 1
1/6

GAT TCT AGC CAT TGC AAG GAT AAA TCT CAG ATA TGC AGC ATC GAT ACA	
Asp Ser Ser His Cys Lys Asp Lys Ser Gln Ile Cys Ser Ile Asp Thr	
480	
* AGT TTT GAG GAA ATA CAA AGA TTT GAT CTC AAA AGG GGC ATG ACT TTG	
Ser Phe Phe Glu Glu Ile Gln Arg Phe Asp Leu Lys Arg Gly Met Thr Leu	
540	
* ATT CTT GAA AAG CAA TGG AGA CAA TTC ATA CAA TTG GCT ATC GTA TTG	
Ile Leu Glu Glu Lys Gln Gln Trp Arg Gln Phe Ile Gln Leu Ala Ile Val Leu	
600	
* GTT TGC ACA TTT GTT ATC GTT CCC AGA GTT GAT GCC GTT GAT GCT CTT	
Val Cys Thr Phe Val Val Ile Val Pro Arg Val Asp Ala Val Asp Ala Leu	
660	
* AAA ACT TGT GCT TGT TTA CTC AAA GAA TGC AGG ATT GAG CTT GCA AAA	
Lys Thr Cys Cys Ala Cys Leu Leu Cys Leu Lys Glu Cys Arg Ile Glu Leu Ala Lys	
TGT ATA GCA AAC CCA TCT TGT GCG GCA AAC GTT GCC TGT CTA CAG ACT	
Cys Ile Ala Asn Pro Ser Cys Ala Ala Asn Val Ala Cys Leu Gln Thr	
720	
* TGC AAC AAT CGT CCT GAC GAG ACC GAA TGT CAG ATA AAA TGT GGT GAC	
Cys Asn Asn Arg Pro Asp Glu Thr Glu Cys Gln Ile Lys Cys Gly Asp	

2/6

780									
* TTC TTC GAA AAC AGT GTG GTG GAC CAA TTC AAC GAG TGT GCG GTT TCC Leu Phe Glu Asn Ser Val Val Asp Gln Phe Asn Glu Cys Ala Val Ser									
840									
* CGA AAG AAA TGT GTG CCC CGG AAA TCG GAT GTG GGT GAA TTC CCG GTT Arg Lys Lys Cys Val Pro Arg Lys Ser Asp Val Glu Phe Pro Val									
900									
* CCG GAT CGT AAT GCA GTG GTT CAA AAT TTT AAC ATG AAA GAC TTT AGT Pro Asp Arg Asn Ala Val Val Gln Asn Phe Asn Met Lys Asp Phe Ser									
GGG AAG TGG TAT ATA ACA AGT GGT TTA AAT CCT ACA TTT GAT GCA TTT Gly Lys Trp Tyr Ile Thr Ser Gly Leu Asn Pro Thr Phe Asp Ala Phe									
960									
* GAT TGT CAA CTT CAT GAG TTT CAT ATG GAA AAT GAT AAA CTT GTT GGG Asp Cys Gln Leu His Glu Phe His Met Glu Asn Asp Lys Leu Val Gly									
1020									
* AAC TTA ACA TGG CGC ATA AAA ACT TTT GAT GGT GGT TTC TTT ACT CGA Asn Leu Thr Trp Arg Ile Lys Thr Leu Asp Gly Gly Phe Thr Arg									
1080									
* TCT GCT GTG CAA ACA TTT GTT CAA GAT CCA GAT CTT CCT GGA GCA CTT Ser Ala Val Gln Thr Phe Val Gln Asp Pro Asp Leu Pro Gly Ala Leu									

FIGURE 1
3/6

1140 *
TAT AAT CAT GAC AAT GAG TTT CTT CAC TAC CAA GAT GAC TGG TAC ATA
Tyr Asn His Asp Asn Glu Phe Leu His Tyr Gln Asp Asp Trp Tyr Ile

TTA TCT TCC CAA ATC GAA AAC AAA CCC GAT GAT TAC ATA TTC GTA TAC
Leu Ser Ser Gln Ile Glu Asn Lys Pro Asp Asp Tyr Ile Phe Val Tyr

1200 *
TAC CGA GGT CGA AAC GAC GCA TGG GAT GGA TAC GGT GGG TCC GTG ATC
Tyr Arg Gly Arg Asn Asp Ala Trp Asp Gly Tyr Gly Ser Val Ile

1260 *
TAC ACC CGA AGC CCG ACA CTC CCC GAA TCG ATC ATC CCA AAC CTA CAA
Tyr Thr Arg Ser Pro Thr Leu Pro Glu Ser Ile Ile Pro Asn Leu Gln

1320 *
AAA GCA GCC AAA TCC GTG GGT CGA GAC TTT AAC AAT TTC ATA ACA ACC
Lys Ala Ala Lys Ser Val Gly Arg Asp Phe Asn Asn Phe Ile Thr Thr

1380 *
GAC AAT AGT TGT GGG CCT GAG CCT CCA TTG GTG GAA AGG CTT GAG AAA
Asp Asn Ser Cys Gly Pro Glu Pro Pro Leu Val Glu Arg Leu Glu Lys

ACA GCG GAA GAG GGC GAG AAG TTG TTG ATA AAA GAA GCT GTA GAG ATA
Thr Ala Glu Glu Gly Glu Lys Leu Leu Ile Lys Glu Ala Val Glu Ile

FIGURE 1
4/6

1440
*
GAA GAG GTT GAA AAA GAG GTG GAG AAG GTT AGA GAT ACT GAG ATG
Glu Glu Glu Val Glu Lys Glu Val Glu Lys Val Arg Asp Thr Glu Met
1500
*
ACT TTG TTT CAG AGG TTG CTT GAA GGG TTT AAG GAG TTG CAA CAA GAT
Thr Leu Phe Gln Arg Leu Glu Leu Glu Lys Glu Leu Gln Asp
1560
*
GAA GAG AAT TTT GTG AGG GAG TTT AGT AAA GAA GAG AAG GAA ATT CTG
Glu Glu Asn Phe Val Arg Glu Leu Ser Lys Glu Lys Glu Ile Leu
1620
*
AAT GAA CTT CAA ATG GAA GCG ACT GAA GTT GAA AAG CTT TTT GGG CGC
Asn Glu Leu Gln Met Glu Ala Thr Glu Val Glu Lys Leu Phe Gly Arg
1680
*
GCG TTA CCG ATT AGG AAA CTT AGA TAAATTT CGATGATTGA TTCAGACAAT
Ala Leu Pro Ile Arg Lys Leu Arg
1740
*
ATATATAGTC ATATGGATTA TGTAGATACT AGAGAAAACC CAAAAAACT TTTGTATACG
1800
*
TGATAAACCGT GTTTGTGATT TGTTTATTGG CTTAAAAATTG TAGAATAGCT TTTTAAATTC

FIGURE 1
5/6

TTTACAAAAA	AATTGATTGT	CTATTGGTAG	CCAAGAGGTT	CACGAAAAAG	CTGAAAAGGGT	1860 *
CTTGCCGGT	TTGCGGGTTA	GGCCAAATT	TTTGGGGCGG	GATCGGTCTT	GATCGGGTTTT	1920 *
TCCTTAAAA	CATGTATTTT	TTATAAATGA	TGAGTTATTT	TCAATTTTGT	GCTAAAAAAA	1980 *

1981
* A

FIGURE 1
6/6

864050-662060

TATTTTCATG	AGTTTGCAGT	TGGTGGTAAT	ACGGTTGAAG	A	ATG	GCT	CTT	GCC	CCT	56						
					Met	Ala	Leu	Ala	Pro	5						
										1						
CAT	TCA	AAT	TTT	CTG	GCC	AAC	CAT	GAA	ACC	ATC	AAA	TAT	TAT	GTT	GGG	104
His	Ser	Asn	Phe	Leu	Ala	Asn	His	Glu	Thr	Ile	Lys	Tyr	Tyr	Val	Gly	20
																15
																10
																25
TCA	AAG	CTT	CCC	GGT	CAT	AAA	AGG	TTT	AGC	TGG	GGT	TGG	GAA	GAT	TAC	152
Ser	Lys	Leu	Pro	Gly	His	Lys	Arg	Phe	Ser	Trp	Gly	Trp	Glu	Asp	Tyr	35
																30
																45
TTT	GGT	AGT	ATA	GTC	GTA	GCA	AAA	ATT	TGT	TCC	AGC	AGA	CGG	ATA	CCT	200
Phe	Gly	Ser	Ile	Val	Val	Ala	Lys	Ile	Cys	Ser	Ser	Arg	Arg	Ile	Pro	50
																40
																55
AGA	TAC	TTT	CGA	AAA	TCT	CCT	AGA	ATA	TGC	TGT	GGT	TTG	GAT	TCA	AGA	248
Arg	Tyr	Phe	Arg	Lys	Ser	Pro	Arg	Ile	Cys	Cys	Gly	Leu	Asp	Ser	Arg	65
																60
																75
GGT	CTG	CAA	CTA	TTC	TCA	CAC	GGG	AAA	CAC	AAT	CTC	TCT	CCC	GCA	CAT	296
Gly	Leu	Gln	Leu	Phe	Ser	His	Gly	Lys	His	Asn	Leu	Ser	Pro	Ala	His	85
																70
																90
AGC	ATT	AAC	CAG	AAT	GTA	CCT	AAG	GGA	AAT	TCA	GGA	TGC	AAA	TTT	CCA	344
Ser	Ile	Asn	Gln	Asn	Val	Pro	Lys	Gly	Asn	Ser	Gly	Cys	Lys	Phe	Pro	100
																95

FIGURE 2
1/5

AAA GAT GTA GCT TTG ATG GTT TGG GAG AAA TGG GGC CAA TTT GCC AAA Lys Asp Val Ala Leu Met Val Trp Glu Lys Trp Gly Gln Phe Ala Lys	105 110 115	392
ACA GCA ATT GTA GCT ATA TTC ATT TTG TCA GTT GCT TCA AAA GCT GAT Thr Ala Ile Val Ala Ile Phe Ile Leu Ser Val Ala Ser Lys Ala Asp	120 125 130	440
GGC GTT GAT GCT CTC AAG ACT TGT ACT TGC TTA CTG AAA GAG TGC AGG Ala Val Asp Ala Leu Lys Thr Cys Thr Cys Leu Leu Lys Glu Cys Arg	135 140 145	488
TTA GAG CTT GCG AAG TGC ATT TCG AAC CCT GCA TGT GCA GCT AAT GTT Leu Glu Leu Ala Lys Cys Ile Ser Asn Pro Ala Cys Ala Ala Asn Val	150 155 160 165	536
GCC TGT CTC CAG ACT TGC AAC AAT AGA CCT GAC GAA ACG GAA TGT CAG Ala Cys Leu Gln Thr Cys Asn Asn Arg Pro Asp Glu Thr Glu Cys Gln	170 175 180	584
ATA AAA TGT GGT GAT TTG TTT GAA AAC AGT GTC GTA GAC GAG TTC AAT Ile Lys Cys Gly Asp Leu Phe Glu Asn Ser Val Val Asp Glu Phe Asn	185 190 195	632
GAG TGT GCA GTC TCC CGA AAG AAA TGT GTA CCT CGT AAA TCT GAT GTT Glu Cys Ala Val Ser Arg Lys Lys Cys Val Pro Arg Lys Ser Asp Val	200 205 210	680

Sequence Alignment

GGT GAC TTT CCT GTA CCT GAT CCC AGT GTT CTT GTC CAG AAG TTT GAC Gly Asp Phe Pro Val Pro Asp Pro Ser Val Leu Val Gln Lys Phe Asp 215 220 225	728
ATG AAA GAT TTT AGC GGG AAA TGG TTC ATT ACT CGC GGT TTG AAT CCC Met Lys Asp Phe Ser Gly Lys Trp Phe Ile Thr Arg Gly Leu Asn Pro 230 235 240 245	776
ACT TTT GAT GCT TTT GAT TGC CAA TTG CAT GAG TTC CAT ACA GAA GAA Thr Phe Asp Ala Phe Asp Cys Gln Leu His Glu Phe Thr Glu Glu 250 255 260	824
AAC AAA CTT GTG GGG AAT TTA TCT TGG AGA ATA CGT ACA CCT GAT GGA Asn Lys Leu Val Gly Asn Leu Ser Trp Arg Ile Arg Thr Pro Asp Gly 265 270 275	872
GGA TTT TTT ACT CGA TCA GCG GTG CAA AAA TTC GTG CAA GAT CCA AAG Gly Phe Phe Thr Arg Ser Ala Val Gln Lys Phe Val Gln Asp Pro Lys 280 285 290	920
TAT CCG GGG ATA CTC TAC AAT GAT AAT AAT AAT AAT AAT AAT AAT AAT Tyr Pro Gly Ile Leu Tyr Asn His Asp Asn Glu Tyr Leu Leu Tyr Gln 295 300 305	968
GAT GAC TGG TAT ATT TTG TCA TCC AAA GTA GAA AAT AGT CCA GAG GAT Asp Asp Trp Tyr Ile Leu Ser Ser Lys Val Glu Asn Ser Pro Glu Asp 310 315 320 325	1016

FIGURE 2
3/5

TAC ATA TTT GTG TAC TAT AAG GGC AGA AAT GAT GCA TGG GAT GGA TAT Tyr Ile Phe Val 330 Tyr Tyr 335 Asn Asp Ala Trp Asp Gly Tyr 340	1064
GGT GGT TCT GTA CTT TAC ACA AGA AGT GCA GTT TTG CCT GAA AGC ATT Gly Gly Ser Val 345 Thr Tyr Thr Arg Ser Ala Val Leu Pro Glu Ser Ile 355	1112
ATA CCG GAG TTG CAA ACC GCA GCT CAA AAA GTT GGG CGT GAT TTC AAC Ile Pro Glu Leu 360 Thr Gln Thr Ala 365 Gln Lys Val Gly Arg Asp Phe Asn 370	1160
ACA TTC ATA AAA ACA GAC AAT ACA TGT GGC CCT GAA CCT CCC CTT GTT Thr Phe Ile Lys Thr Asp Asn Thr Cys Gly Pro Glu Pro Pro Leu Val 385	1208
GAG AGG TTG GAG AAG AAA AAG GTG GAA GAA GGA GAA AGG ACG ATC ATA AAA Glu Arg Leu Glu Lys 390 Lys Lys 395 Glu Val Glu Glu Gly 400 Glu Arg Thr Ile Ile Lys 405	1256
GAA GTT GAG GAG ATA GAA GAA GAA GAA GAA GAA GAA GAA GAA GAA GAA Glu Val Glu Glu Ile Glu Glu Glu Glu Glu Glu Lys Val Arg Asp Lys Glu 410 415 420	1304
GTC ACC TTA TTC AGT AAA CTG TTT GAA GGT TTT AAA GAG CTC CAA CGA Val Thr Leu Phe Ser Lys Lys Leu Phe Glu Glu Lys Glu Leu Gln Arg 425 430 435	1352

GAT GAA GAG AAC TTC TTA AGA GAG CTG AGC AAA GAA GAA ATG GAT GTT	1400
Asp Glu Glu Asn Phe Leu Arg Glu Leu Ser Lys Glu Glu Met Asp Val	
440	445
	450
TTG GAT GGA CTT AAA ATG GAA GCA ACT GAG GTA GAA AAA CTT TTT GGG	1448
Leu Asp Gly Leu Lys Met Glu Ala Thr Glu Val Glu Lys Leu Phe Gly	
455	460
	465
CGT GCT TTA CCA ATA AGG AAA TTA A GGTAAGT ATTTTAAAAA CTATCAACAT	1500
Arg Ala Leu Pro Ile Arg Lys Leu	
470	475
ATATACTACA TGTATAGTTG TATTGATTG TTTTGCCCTGG AATAGATTGC TTATACATCA	1560
TGTATTGCTT CTTTTTCAGA AGCAAAAAA	1589

Sequence

CCACGCGTCC	GGCTTGGTGT	GGGGAAGATT	AGATAGTGTG	AAGA	ATG	GCA	GTA	GCT	56
					Met	Ala	Val	Ala	
									1
ACA CAT TGT TTC ACT TCA CCT TGT CAT GAC CGT ATT CGA TTT TTC TCA									104
Thr His Cys Phe Thr Ser Pro Cys His Asp Arg Ile Arg Phe Ser									20
5	10	15	20						
AGT GAT GAT GGT ATT GGT AGG CTT GGC ATT ACA AGA AAG AGG ATC AAT									152
Ser Asp Asp Gly Ile Gly Arg Leu Gly Ile Thr Arg Lys Arg Ile Asn									35
25	30								
GGC ACT TTC TTG CTC AAG ATT TTA CCT CCA ATC CAA AGT GCT GAT CTC									200
Gly Thr Phe Leu Leu Lys Ile Leu Pro Pro Ile Gln Ser Ala Asp Leu									50
40	45								
AGA ACA ACT GGT GGT GGG AGA TCC TCA CGT CCT TTA TCT GCA TTC AGG TCA									248
Arg Thr Thr Gly Gly Arg Ser Ser Arg Pro Leu Ser Ala Phe Arg Ser									65
55	60								
GGA TTC TCT AAG GGG ATA TTT GAC ATT GTG CCA TTA CCA TCA AAG AAT									296
Gly Phe Ser Lys Gly Ile Phe Asp Ile Val Pro Leu Pro Ser Lys Asn									80
70	75								
GAG CTG AAA GAG CTG ACC GCT CCG CTG TTG CTA AAA CTC GTG GGT GTT									344
Glu Leu Lys Glu Leu Thr Ala Pro Leu Leu Leu Lys Leu Val Gly Val									100
85	90								

FIGURE 3
1/5

Sequence alignment

TTA GCT TGC GCG TTC CTT ATT GTT CCA TCT GCA GAT GCA GTT GAT GCA	392
Leu Ala Cys Ala Phe 105	
Leu 110	
CTT AAA ACT TGT GCA TGC TTA TTG AAG GGA TGC AGG ATA GAA CTC GCA	440
Leu Lys Thr Cys Ala 120	
Leu 125	
AAG TGC ATT GCC AAC CCT GCC TGT GCA GCC AAT GTC GCG TGC CTT CAG	488
Lys Cys Ile Ala Asn Pro Ala 135	
Leu 140	
ACC TGC AAT AAC CGT CCA GAT GAA ACC GAG TGC CAG ATT AAA TGT GGG	536
Thr Cys Asn Asn Arg Pro Asp 150	
Leu 155	
GAT CTG TTT GAG AAC AGT GTT GAT GAT GAG TGC AAC GAG TGT GCT GTG	584
Asp Leu Phe Glu Asn Ser Val 165	
Leu 170	
TCG AGA AAA AAG TGT GTT CCT CCT AGA AAA TCT GAT CTC GGA GAA TTT CCT	632
Ser Arg Lys Lys Cys Val 185	
Leu 190	
GCC CCA GAC CCT TCT GTT CTT GTA CAG AAC TTC AAC ATC TCG GAC TTT	680
Ala Pro Asp Pro Ser 200	
Leu 205	
Leu 210	

FIGURE 3
2/5

Sequence 33333

AAC GGG AAG TGG TAC ATT ACA AGT GGC TTG AAT CCA ACC TTT GAT GCC	728
Asn Gly Lys Trp Tyr Trp Ser Gly Leu Asn Pro Thr Phe Asp Ala	
215 220 225	
TTC GAC TGC CAG CTG CAT GAG TTC CAC ACA GAA GGT GAC AAC AAG CTT	776
Phe Asp Cys Gln Leu His Glu Phe His Thr Glu Gly Asp Asn Lys Leu	
230 235 240	
GTT GGA AAC ATC TCT TGG AGA ATA AAG ACC CTA GAC AGT GGA TTC TTT	824
Val Gly Asn Ile Ser Trp Arg Ile Lys Thr Leu Asp Ser Gly Phe	
245 250 255 260	
ACT AGG TCA GCC GTA CAA AAA TTC GTG CAA GAT CCT AAC CAA CCT GGT	872
Thr Arg Ser Ala Val Gln Lys Phe Val Gln Asp Pro Asn Gln Pro Gly	
265 270 275	
GTT CTC TAC AAT CAT GAC AAC GAG TAC CTT CAC CAC TAT CAA GAT GAC TGG	920
Val Leu Tyr Asn His Asp Asn Glu Tyr Leu His Tyr Gln Asp Asp Trp	
280 285 290	
TAT ATC CTG TCA TCA AAG ATA GAG AAT AAA CCT GAA GAC TAT ATA TTT	968
Tyr Ile Leu Ser Ser Ser Lys Ile Glu Asn Lys Pro Glu Asp Tyr Ile Phe	
295 300 305	
GTA TAC TAC CGT GGG CGA AAC GAT GCT TGG GAT GGA TAT GGT GGT GCA	1016
Val Tyr Tyr Arg Gly Arg Asn Asp Ala Trp Asp Gly Tyr Gly Ala	
310 315 320	

362333-362333

GTT GTA TAC ACG AGA AGT TCT GTA TTA CCC AAT AGC ATT ATA CCA GAA 1064
Val Val Tyr Thr Arg Ser Ser Val Leu Pro Asn Ser Ile Ile Pro Glu 340
325 330 335

CTC GAA AAA GCA GCA AAA AGC ATA GGC AGA GAC TTC AGC ACA TTC ATT 1112
Leu Glu Lys Ala Ala Lys Ser Ile Gly Arg Asp Phe Ser Thr Phe Ile 355
345 350

AGA ACG GAT AAC ACA TGT GGT CCT GAA CCT GCG CTC GTG GAG AGA ATT 1160
Arg Thr Asp Asn Thr Cys Gly Pro Glu Pro Ala Leu Val Glu Arg Ile 370
360 365

GAG AAG ACA GTG GAA GAA GGT GAA AGG ATA ATC GTA AAA GAG GTT GAA 1208
Glu Lys Thr Val Glu Glu Gly Glu Arg Ile Ile Val Lys Glu Val Glu 385
375 380

GAG ATA GAA GAA GAG GTA GAG AAG GAA GTG GAG AAG GTC GGT AGG ACT 1256
Glu Ile Glu Glu Glu Val Glu Lys Glu Val Glu Lys Val Gly Arg Thr 400
390 395

GAG ATG ACC TTG TTC CAG AGA TTG GCT GAA GGA TTT AAT GAA CTG AAG 1304
Glu Met Thr Leu Phe Gln Arg Leu Ala Glu Gly Phe Asn Glu Leu Lys 420
405 410 415

CAA GAC GAG GAG AAT TTC GTG AGA GAG TTA AGT AAA GAA GAG ATG GAG 1352
Gln Asp Glu Glu Asn Phe Val Arg Glu Leu Ser Lys Glu Glu Met Glu 435
425 430

TTT TTG GAT GAG ATC AAA ATG GAA CCA AGT GAG GTT GAA AAA TTG TTT	1400
Phe Leu Asp Glu Ile Lys Met Glu Ala Ser Glu Val Glu Lys Leu Phe	
440	445
	450
GGG AAA GCT TTG CCA ATC AGG AAG GTC AGG TAGAAACAAG AACCCACATT	1450
Gly Lys Ala Leu Pro Ile Arg Lys Val Arg	
455	460
GTTGTACAAA CTATATTATA CATACTGTGT TCGGTTTCATA TAAAGTAATA TTTTGTGACA	1510
CAGTCATCAT CATTCCATAA CAATTGGATA AAAAAAAAAA AAAAAA	1555

FIGURE 3
5/5

Tobacco	MALAPHSNFLANHETIKYYVGSGLPGHKRFSWGWEDYFGSIVVAKICSSR	50
Arabidopsis	M-V-T-.....CFT-PCHDRI--FSS.D-GI-RLGITRK....	33
Lettuce	M--SL-TV--CKE-ALNL-AR-PCNE...--HRS.GQPPTN-IMM--....	43
Tobacco	RIPRYFRKSPRICCGLDSEGLQLF.SHGKHNLSPAHSINQNVPKGNSGCK	99
Arabidopsis	--NGT-L..LK-LPPIQ-AD-RTTGGRSSRP--AFR-GFSKGIFDIVPLP	81
Lettuce	-SNNGYFN-F-LFTSYKTSSF..SD-SHCKDK-QI.CSIDTSFEEIQRFD	90
Tobacco	FPKDVALMVWEKWQFAKTAIVAIFILSVASKADA	134
Arabidopsis	SKNELKELTA...PLLL-LVG-LACAFILVPS---	113
Lettuce	LKRGMT-ILEKQ-R--IQL---LVCTFVIVPRV--	125
Tobacco	VDALKTCTCLLKECRLELAKCISNPACAAVACLQTCNNRPDETECQIKC	50
Arabidopsis	-----A-----G--I-----A-----	50
Lettuce	-----A-----I-----A--S-----	50
Tobacco	GDLFENSVVDEFNECAVSRKKCVPRKSDVGDFPVDPDPSVLVQKFDMDKDFS	100
Arabidopsis	-----I-E--A-----N-NIS--N	100
Lettuce	-----Q-----E-----RNAV--N-N----	100
Tobacco	GKWFITRGLNPTFDAFDCQLHEFHTE.ENKLVGNLSWRIRTPDGGFFTRS	149
Arabidopsis	---Y--S-----GD-----I---K-L-S-----	150
Lettuce	---Y--S-----M-ND.-----T---K-L-----	149
Tobacco	AVQKFVQDPKYPGILYNHDNEYLLYQDDWYILSSKVENSPEDYIFVYYKG	199
Arabidopsis	-----NQ--V-----H-----I--K-----R-	200
Lettuce	---T---DL--A-----F-H-----QI--K-D-----R-	199
Tobacco	RNDAWDGYGGSVLYTRSAVLPESIIPELQTAAQKVGRDFNTFIKTNDTCG	249
Arabidopsis	-----A-V---S---N-----EK--KSI---S---R-----	250
Lettuce	-----I---PT-----N--K--KS-----N--T---S--	249
Tobacco	PEPPIVERLEKKVEEGERTIIKEVEEIEE...EVEKVRDKEVTLFSKLF	295
Arabidopsis	---A---I---T-----I-V-----EVEK-----GRT-M---QR-A	300
Lettuce	-----TA---KLL---AV---EVEK-----T-M---QR-L	299
Tobacco	EGFKEIQRDEENFLRELSKEEMDVL.DGLKMEATEVEKLFGRALPIRKLK	344
Arabidopsis	---N--KQ---V-----EF--EI---S-----K-----V-	349
Lettuce	-----Q---V-----KEI-NE-Q-----	348



A Cysteine-rich domain

B Lipocalin signature

C Highly charged domain

FIGURE 4

Percent Identity and Similarity* of Pre-protein VDE

	Lettuce	Tobacco	Arabidopsis
Lettuce		67 (78)	69 (82)
Tobacco	69	protein cDNA	68 (81)
Arabidopsis	66		68

*similarity values are in parentheses

Percent Identity and Similarity* of Mature VDE

	Lettuce	Tobacco	Arabidopsis
Lettuce		82 (90)	83 (91)
Tobacco	76	protein cDNA	83 (92)
Arabidopsis	74		77

*similarity values are in parentheses

FIGURE 5

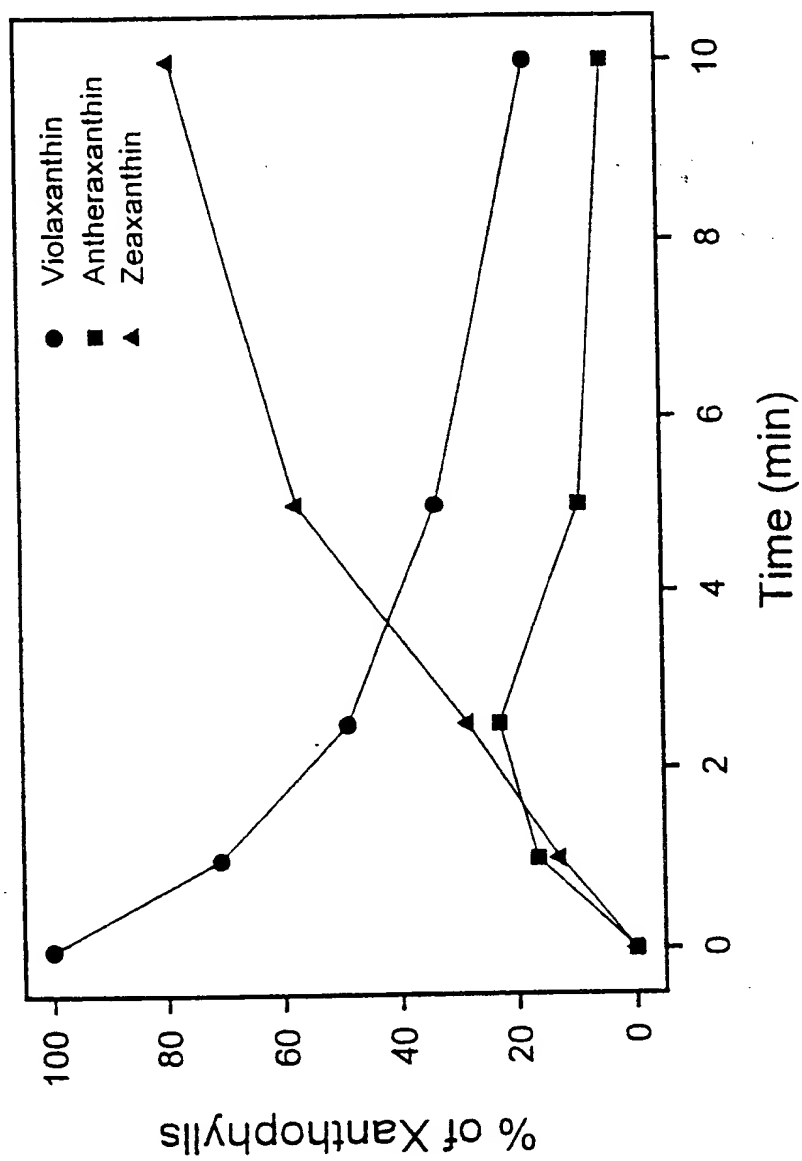
[illegible]

FIGURE 7A

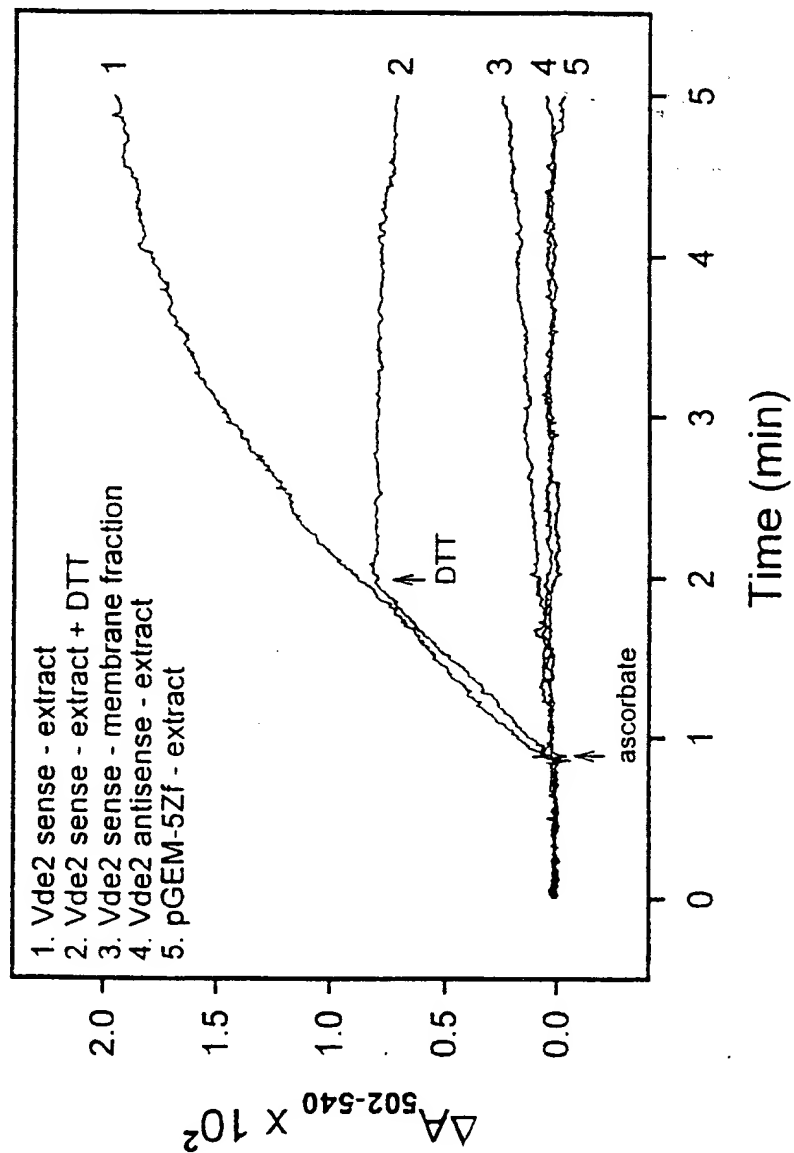


FIGURE 7B

Plant	Treatment	N	V	A	Z	V+A+Z	L	Chlb/Chla	$\beta\beta$ -Carotene	%V Deepoxidized
Ct-11	Dark	77.13	64.67	1.54	0	66.21	335.12	0.39	136.95	
	Light	77.65	25.56	6.25	30.93	62.74	338.15	0.40	131.76	60.5
Ct-14	Dark	71.60	77.74	1.19	0	78.93	312.05	0.36	150.08	
	Light	72.00	29.07	7.97	43.07	80.11	311.36	0.37	151.50	62.6
Ct-15	Dark	76.68	67.44	0	0	67.44	345.73	0.43	130.05	
	Light	74.45	26.73	7.78	37.44	71.95	337.87	0.42	126.36	60.4
Ct-18	Dark	68.28	82.55	2.33	0	84.88	298.36	0.35	136.67	
	Light	69.65	34.50	13.25	38.44	86.19	311.07	0.36	138.95	58.2
Ct-20	Dark	78.45	70.60	2.85	0	73.45	351.57	0.39	139.58	
	Light	77.38	23.14	5.46	42.66	71.26	343.25	0.39	133.61	67.2
Ct-22	Dark	72.68	104.14	3.40	0	107.54	323.93	0.37	138.29	
	Light	72.13	27.63	6.62	78.66	112.91	315.07	0.40	128.30	73.5
Ct-24	Dark	70.77	76.82	1.55	0	78.37	334.20	0.43	132.95	
	Light	76.52	29.35	7.92	45.24	82.51	339.60	0.44	131.55	61.8
Ct-26	Dark	75.28	63.41	0	0	63.41	346.45	0.44	130.38	
	Light	77.34	26.27	6.16	34.19	66.62	346.91	0.44	128.27	58.6
Ct-30	Dark	78.23	59.66	1.73	0	61.39	357.63	0.45	127.62	
	Light	79.37	26.47	4.93	31.61	63.01	352.39	0.46	124.80	55.6
Ct-31	Dark	71.72	75.91	1.74	0	77.65	315.40	0.37	144.24	
	Light	73.00	31.43	8.74	37.65	77.82	312.80	0.38	145.13	58.6
Ct-39	Dark	75.99	77.93	0	0	77.93	335.79	0.43	127.17	
	Light	74.79	26.28	8.07	41.30	75.65	331.35	0.42	123.11	66.3
Ct-40	Dark	77.56	79.07	2.99	0	82.06	358.33	0.44	126.05	
	Light	77.78	27.44	10.10	47.92	85.46	352.66	0.43	120.89	65.3

Mean = 62.4 ± 5.0

N = 9'-cis-neoxanthin V = violaxanthin A = antheraxanthin Z = zeaxanthin L = lutein Chla = chlorophyll a Chlb = chlorophyll b
All values are relative to chlorophyll a (mmol mol⁻¹ Chla) except Chlb/Chla which is (mol/mol).

FIGURE 8
1 OF 3

Plant	Treatment	N	V	A	Z	V+A+Z	L	Chlb/Chla	88-Carotene	%V De-epoxidized	% Inhibition of De-epoxidation
TAS-32	Dark	74.19	76.98	0	0	76.98	325.75	0.42	136.45		94.1
	Light	73.78	74.15	2.18	0	76.33	330.95	0.41	131.73	3.7	
TAS-39	Dark	77.92	59.19	0	0	59.19	329.29	0.41	141.45		92.5
	Light	75.06	56.39	2.70	0	59.09	322.29	0.40	141.52	4.7	
TAS-21	Dark	75.78	53.19	0	0	53.19	335.21	0.45	132.85		72.0
	Light	77.92	43.90	7.30	9.37	60.57	326.90	0.45	130.33	17.5	
TAS-5	Dark	67.82	79.21	3.43	0	82.64	300.82	0.39	139.00		65.9
	Light	69.72	62.31	14.66	8.27	85.24	300.63	0.40	137.13	21.3	
TAS-17	Dark	74.89	64.54	1.08	0	65.62	317.69	0.41	143.42		63.6
	Light	74.00	49.89	8.49	8.53	66.91	325.32	0.40	139.28	22.7	
TAS-13	Dark	77.92	49.33	1.27	0	50.60	339.63	0.45	135.36		62.7
	Light	78.02	37.82	4.94	7.18	49.94	340.45	0.45	132.78	23.3	
TAS-6	Dark	74.42	55.77	0	0	55.77	340.84	0.44	136.77		55.4
	Light	74.95	40.27	9.69	13.99	63.95	332.00	0.44	135.36	27.8	
TAS-37	Dark	73.05	59.18	1.24	0	60.42	323.30	0.39	135.81		45.3
	Light	71.36	38.97	14.48	9.98	63.43	313.46	0.38	134.62	34.1	
TAS-3	Dark	74.04	60.25	1.76	0	62.01	319.39	0.43	138.89		44.2
	Light	76.98	39.26	7.41	14.33	61.00	322.14	0.44	136.00	34.8	
TAS-36	Dark	69.77	77.86	1.42	0	79.28	295.52	0.36	151.33		40.1
	Light	70.74	48.73	12.76	12.81	74.30	308.06	0.36	151.35	37.4	
TAS-35	Dark	75.59	63.24	1.05	0	64.29	342.09	0.42	130.30		39.7
	Light	75.76	39.48	10.38	17.49	67.35	337.57	0.42	128.88	37.6	
TAS-4	Dark	73.61	68.23	1.31	0	69.54	321.12	0.42	135.43		38.6
	Light	73.23	42.07	8.95	17.84	68.86	320.33	0.42	131.73	38.3	
TAS-9	Dark	72.28	52.57	1.75	0	54.32	324.02	0.42	140.21		36.4
	Light	73.28	31.72	6.19	18.59	56.50	317.11	0.42	136.93	39.7	
TAS-7	Dark	72.55	71.02	1.81	0	72.83	321.37	0.40	133.21		

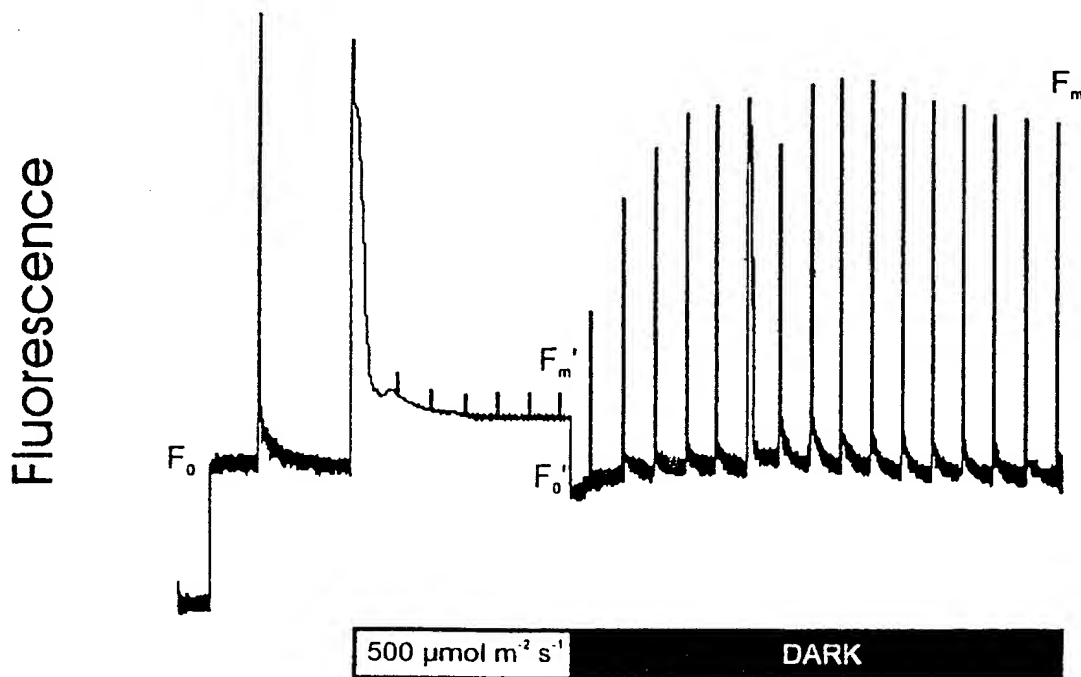
FIGURE 8
N OF 3

TAS-38	Light	71.79	39.82	14.04	21.09	74.95	322.04	0.40	130.57	43.9	29.6
	Dark	71.66	61.97	1.77	0	63.74	329.67	0.41	135.87		
TAS-16	Light	73.24	34.45	8.83	19.57	62.85	331.17	0.41	133.77	44.4	28.8
	Dark	72.15	62.54	2.04	0	64.58	329.72	0.41	135.12		
TAS-18	Light	74.04	33.28	9.10	23.83	66.21	335.60	0.42	131.32	46.8	25.0
	Dark	75.09	59.64	1.72	0	61.36	345.04	0.42	127.38		
TAS-34	Light	75.26	31.68	7.11	23.01	61.80	340.79	0.42	126.85	46.9	24.8
	Dark	72.35	65.39	1.79	0	67.18	326.06	0.41	131.12		
	Light	71.25	34.26	9.26	30.41	73.93	316.49	0.42	128.96	47.6	23.7

N = 9'-cis-neoxanthin V = violaxanthin A = antheraxanthin Z = zeaxanthin L = lutein Chla = chlorophyll a Chlb = chlorophyll b

All values are relative to chlorophyll a (mmol mol⁻¹ Chla) except Chlb/Chla which is (mol/mol).

Ct-30

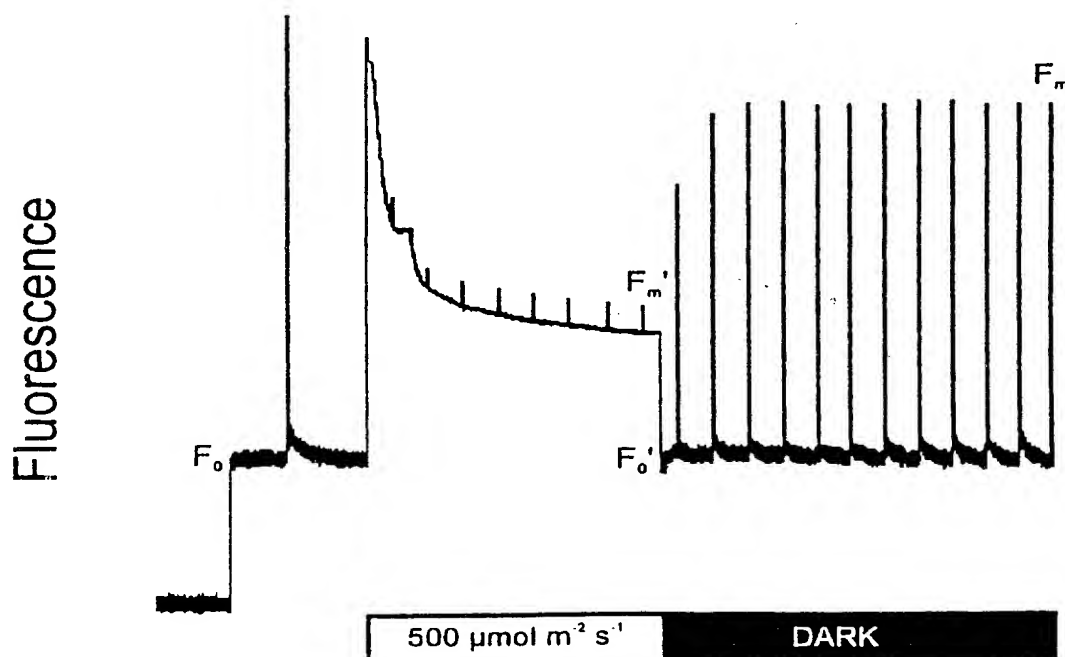


	Dark-adapted	Pre-illuminated	Post-fluorescence Analysis
V	64.28	51.77	44.98
A	1.99	6.16	11.10
Z	0	10.17	13.77
V+A+Z	66.27	68.10	69.85
De-epoxidation (%)		19.5	30.00
(Fm/Fm') - 1			2.20
(Fo/Fo') - 1			0.15

All values are relative to chlorophyll a ($\text{mmol mol}^{-1} \text{Chla}$).

FIGURE 9

TAS-5



	Dark-adapted	Pre-illuminated	Post-fluorescence Analysis
V	67.51	NA	65.38
A	0	NA	2.14
Z	0	NA	0
V+A+Z	67.51	NA	67.52
De-epoxidation (%)		NA	3.20
(Fm/Fm') - 1			1.34
(Fo/Fo') - 1			0

All values are relative to chlorophyll a ($\text{mmol mol}^{-1} \text{Chla}$).

NA - Not assayed

FIGURE 10